

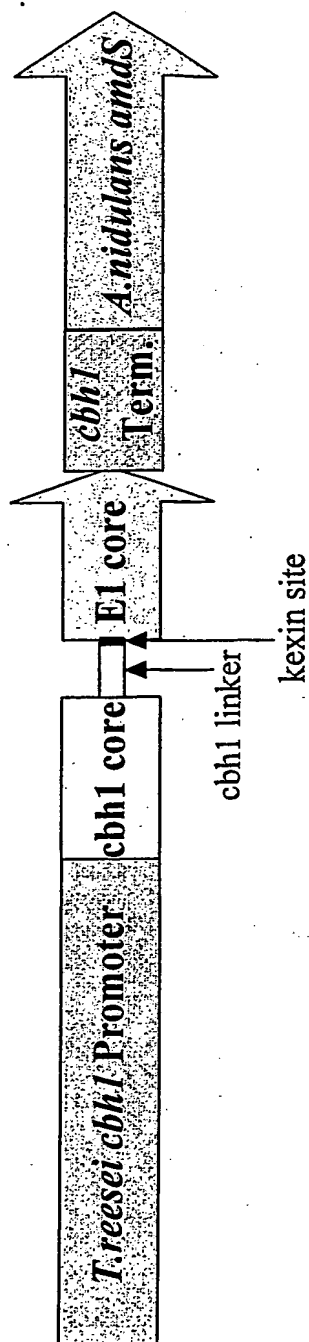
FIGURE 1

CBH1-E1 Fusion Construct

T. reesei cbh1 core, linker (no CBD)

+

Acidothermus cellulolyticus endoglucanase 1 core (E1)



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Figure 2

DNA sequence of *T.reesei cbh1* signal sequence+catalytic domain+linker (1570 bases)

ATGTATCGGAAGTTGGCCGTCATCTCGGCCTTCTTGGCCACAGCTCGTGCTCA
GTCGGCCTGCACTCTCCAATCGGAGACTCACCCGCCTCTGACATGGCAG
AAATGCTCGTCTGGTGGCACTTGCACCTAACAGACAGGCTCCGTGGTCA
TCGACGCCAACTGGCGCTGGACTCACGCTACGAACAGCAGCACGAACTG
CTACGATGGCAACACTTGGAGCTCGACCCTATGTCCTGACAACGAGACC
TGCGCGAAGAAGTGTGTCTGGACGGTGCCGCCTACGCGTCCACGTACG
GAGTTACCACGAGCGGTAACAGCCTCTCCATTGGCTTTGTCACCCAGTC
TGCGCAGAAGAACGTTGGCGCTCGCCTTTACCTTATGGCGAGCGACACG
ACCTACCAGGAATTCACCCTGCTTGGCAACGAGTTCTCTTTCGATGTTGA
TGTTTCGCAGCTGCCGTAAGTGACTTACCATGAACCCCTGACGTATCTTC
TTGTGGGCTCCCAGCTGACTGGCCAATTTAAGGTGCGGCTTGAACGGAG
CTCTCTACTTCGTGTCCATGGACGCGGATGGTGGCGTGAGCAAGTATCC
CACCAACACCGCTGGCGCCAAGTACGGCACGGGGTACTGTGACAGCCAG
TGTCCTCCGCGATCTGAAGTTCATCAATGGCCAGGCCAACGTTGAGGGCT
GGGAGCCGTCATCCAACAACGCAAACACGGGCATTGGAGGACACGGAA
GCTGCTGCTCTGAGATGGATATCTGGGAGGCCAACTCCATCTCCGAGGC
TCTTACCCCCCACCCTTGCACGACTGTCGGCCAGGAGATCTGCGAGGGT
GATGGGTGCGGCGGAACTTACTCCGATAACAGATATGGCGGCACTTGCG
ATCCCGATGGCTGCGACTGGAACCCATACCGCCTGGGCAACACCAGCTT
CTACGGCCCTGGCTCAAGCTTTACCCTCGATACCACCAAGAAATTGACC
GTTGTACCCAGTTCGAGACGTCGGGTGCCATCAACCGATACTATGTCC
AGAATGGCGTCACTTTCCAGCAGCCCAACGCCGAGCTTGGTAGTTACTC
TGGCAACGAGCTCAACGATGATTACTGCACAGCTGAGGAGGCAGAATTC
GGCGGATCCTCTTTCTCAGACAAGGGCGGCCTGACTCAGTTCAAGAAGG
CTACCTCTGGCGGCATGGTTCTGGTCATGAGTCTGTGGGATGATGTGAG
TTTGATGGACAAACATGCGCGTTGACAAAGAGTCAAGCAGCTGACTGAG
ATGTTACAGTACTACGCCAACATGCTGTGGCTGGACTCCACCTACCCGA
CAAACGAGACCTCCTCCACACCCGGTGCCGTGCGCGGAAGCTGCTCCAC
CAGCTCCGGTGTCCCTGCTCAGGTCGAATCTCAGTCTCCCAACGCCAAG
GTCACCTTCTCCAACATCAAGTTCGGACCCATTGGCAGCACCGGCAACC
CTAGCGGCGGCAACCCCTCCCGGCGGAAACCCGCCTGGCACCACCACCCCG
CCGCCCAGCCACTACCACTGGAAGCTCTCCCGGACCTACTAGT

Figure 3

Amino acid sequence of *T.reesei cbh1* signal sequence + catalytic domain + linker (480 amino acids)

MYRKLAVISAFLATARAQSACTLQSETHPPLTWQKCSSGGTCTQQTGSVVID
ANWRWTHATNSSTNCYDGNTWSSTLCPDNETCAKNCCLDGAAYASTYGVT
TSGNSLSIGFVTQSAQKNVGARLYLMASDTTYQEFTLLGNEFSFDVDVSQLP
CGLNGALYFVSMADADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQA
NVEGWEPSSNNANTGIGGGHGCCSEMDIWEANSISEALTPHPCTTVGQEICE
GDGCGGTYSNRYGGTCDPDGCDWNPYRLGNTSFYGPSSFTLDTTKKLT
VVTQFETSGAINRYVQNGVTFQQPNAELGSYSGNELNDDYCTAEEAEFGG
SSFSDKGGLTQFKKATSGGMVLVMSLWDDYYANMLWLDSTYPTNETSSTP
GAVRGSCSTSSGVPAQVESQSPNAKVTFESNIKFGPIGSTGNPSGGNPPGGNPPG
TTTTRRPATTTGSSPGPTS

Figure 4

DNA sequence of *Acidothermus cellulolyticus* GH5A endoglucanase 1 catalytic domain
(1077 bases)

GCGGGCGGCGGCTATTGGCACACGAGCGGCCGGGAGATCCTGGACGCGAAC
AACGTGCCGGTACGGATCGCCGGCATCAACTGGTTTGGGTTCGAAACCTGCA
ATTACGTTCGTGCACGGTCTCTGGTCACGCGACTACCGCAGCATGCTCGACCA
GATAAAGTCGCTCGGCTACAACACAATCCGGCTGCCGTACTCTGACGACATT
CTCAAGCCGGGCACCATGCCGAACAGCATCAATTTTACCAGATGAATCAGG
ACCTGCAGGGTCTGACGTCCTTGCAGGTCATGGACAAAATCGTCGCGTACGC
CGGTACAGATCGGCCTGCGCATCATTCTTGACCGCCACCGACCGGATTGCAGC
GGGCAGTCGGCGCTGTGGTACACGAGCAGCGTCTCGGAGGCTACGTGGATTT
CCGACCTGCAAGCGCTGGCGCAGCGCTACAAGGGAAACCCGACGGTCGTCG
GCTTTGACTTGCACAACGAGCCGCATGACCCGGCCTGCTGGGGCTGCGGCGA
TCCGAGCATCGACTGGCGATTGGCCGCCGAGCGGGCCGGAAACGCCGTGCTC
TCGGTGAATCCGAACCTGCTCATTTTCGTCGAAGGTGTGCAGAGCTACAACG
GAGACTCCTACTGGTGGGGCGGCAACCTGCAAGGAGCCGGCCAGTACCCGGT
CGTGCTGAACGTGCCGAACCGCCTGGTGTACTCGGCGCACGACTACGCGACG
AGCGTCTACCCGCAGACGTGGTTCAGCGATCCGACCTTCCCCAACAACATGC
CCGGCATCTGGAACAAGAAGTGGGGATACCTCTTCAATCAGAACATTGCACC
GGTATGGCTGGGCGAATTCGGTACGACACTGCAATCCACGACCGACCAGACG
TGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCGCAATACGGTGCGG
ACAGCTTCCAGTGGACCTTCTGGTCCTGGAACCCCGATTCCGGCGACACAGG
AGGAATTCTCAAGGATGACTGGCAGACGGTCGACACAGTAAAAGACGGCTAT
CTCGCGCCGATCAAGTCGTCGATTTTCGATCCTGTGCGC

Figure 5

Amino acid sequence of *Acidothermus cellulolyticus* GH5A endoglucanase 1 catalytic domain (359 amino acids)

AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYYVHGLWSRDYRSMLDQI
KSLGYNTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIG
LRILDRHRPDCSGQSALWYTSSVSEATWISDLQALAQRKYKGNPTVVGFDLHNEP
HDPACWGCGDPSIDWRLAAERAGNAVLSVNPNNLIFVEGVQSYNGDSYWWGG
NLQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTWFSPTFPNNMPGIWNKNW
GYLFNQNIAPVWLGEFGTTLQSTTDQTLVQYLRPTAQYGADSFQWTFWS
WNPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPVG

FIGURE 6

DNA sequence of *Acidothermus cellulolyticus* GH48 cellulase catalytic domain (1914 bases)

AACGACCCGTACATCCAGCGGTTCTCACGATGTACAACAAGATTCACGACC
CAGCGAACGGCTACTTCAGCCCCGACGGGAATTCCTACCACTCGGTTAGAAAC
GCTCATCGTTGAGGCACCGGACTACGGGCACGAGACAACCTTCGGAGGCGTAC
AGCTTCTGGCTCTGGCTCGAAGCGACGTACGGCGCAGTGACCGGCAACTGGA
CGCCGTTCAACAACGCCTGGACGACGATGGAAACGTACATGATCCCGCAGCA
CGCGGACCAGCCGAACAACGCGTCGTACAACCCCAACAGCCCGGCGTCGTAC
GCTCCGGAAGAGCCGCTGCCCAGCATGTACCCGGTTGCCATCGACAGCAGCG
TGCCGGTTGGGCACGACCCGCTCGCCGCCGAATTGCAGTCGACGTACGGCAC
TCCGGACATTTACGGCATGCACTGGCTGGCCGACGTTGACAACATCTACGGA
TACGGCGACAGCCCCGGCGGTGGTTGCGAACTCGGTCCTTCCGCTAAGGGCG
TCTCCTACATCAACACATTCCAGCGCGGCTCGCAGGAGTCCGTCTGGGAGAC
GGTACCCAGCCGACGTGCGACAACGGCAAGTACGGTGGGGCGCACGGCTA
CGTCGACCTGTTTCATCCAGGGTTTCGACGCCGCCGACGTGGAAGTACACCGAT
GCCCCGGACGCCGACGCCCGTGCCGTCCAGGCTGCGTACTGGGCCTACACCT
GGGCATCGGCGCAGGGCAAGGCAAGCGCGATTGCCCCGACGATCGCCAAGG
CGGCCAAACtCGGCGACTACCTGCGGTACTCGCTCTTTGACAAGTACTTCAAG
CAGGTCGGCAACTGCTACCCGGCCAGCTCCTGCCCTGGAGCAACCGGACGCC
AGAGCGAGACCTACCTGATCGGCTGGTACTACGCCTGGGGCGGCTCAAGCCA
AGGCTGGGCCTGGCGCATTGGTGACGGCGCCGCGCACTTCGGCTACCAGAAT
CCGCTTGCCGCGTGGGCGATGTGCAACGTGACACCGCTCATTCCGCTCTCGCC
CACGGCAAAGAGCGACTGGGCGGCGAGCTTGCAGCGCCAGCTGGAGTTCTAC
CAGTGGTTGCAATCCGCGGAAGGAGCCATTGCGGGCGGCGCCACCAACAGCT
GGAACGGCAATTACGGGACCCCGCCGGCCGGAGACTCGACCTTCTACGGCAT
GGCGTACGACTGGGAGCCGGTCTACCACGACCCGCCGAGCAACAACCTGGTTC
GGCTTCCAGGCGTGGTCCATGGAACGGGTTGCCGAGTACTACTACGTCACCG
GCGACCCGAAGGCCAAGGCGCTGCTCGACAAGTGGGTCGCATGGGTGAAGC
CGAATGTCACCACCGGTGCCTCATGGTTCGATTCCGTTCGAATTTGTCCTGGAGC
GGCCAACCGGATACCTGGAATCCGAGCAACCCAGGAACGAATGCCAACCTG
CACGTGACCATCACGTCGTCCGGGCAGGACGTCCGGTGTGCCGCGGCGCTCG
CGAAGACACTCGAGTACTACGCGGCAAAATCCGGCGATACGGCCTCGCGCGA
CCTCGCGAAGGGATTGCTCGACTCCATGTGGAACAACGACCAGGACAGCCTC
GGTGTGAGCACACCGGAGACGCGGACCGACTACTCTCGGTTCACTCAGGTGT
ACGACCCGACGACTGGTGACGGCCTCTACATCCCGTCGGGTTGGACGGGGAC
CATGCCCAACGGTGACCAAATCAAGCCGGGTGCGACCTTCTGAGCATCCGG
TCCTGGTACACCAAGGATCCGCAAGTGGTTCGAAGGTGCAGGCGTACCTCAACG
GCGGGCCTGCTCCGACGTTCAACTACCACCGGTTCTGGGCGGAGTCCGACTT
CGCGATGGCGAACGCCGATTTTGGCATGCTCTTCCCATCCGGG

FIGURE 7

Amino acid sequence of *Acidothermus cellulolyticus* 48 catalytic domain (638 amino acids)

NDPYIQRFLTMYNKIHPANGYFSPQGIPYHSVETLIVEAPDYGHETTSEAYSFW
LWLEATYGAVTGNWTPFNNAWTTMETYMIPQHADQPNNASYNPNSPASYAPEE
PLPSMYPVAIDSSVPVGHDPAAELQSTYGTPDIYGMHWLADVNDNIYGYGDSFG
GGCELGPSAKGVS YINTFQRGSQESVWETVTQPTCDNGKYGGAHGYVDLFIQGS
TPPWKYTDAPDADARAVQAAYWAYTWASAQGKASAIPTIAKAAKLGDYLR
YSLFDKYFKQVGNCYPASSCPGATGRQSETYLIGWYYAWGGSSQGWAWRIGD
GAAHFGYQNPLAAWAMSNVTPLIPLSPTAKSDWAASLQRQLEFYQWLQSAEGA
IAGGATNSWNGNYGTPPAGDSTFYGMAYDWEVPVYHDPPSNNWFGFQAWSMER
VAEYYYVTGDPKAKALLDKWVAWVKPNVTTGASWSIPSNLSWSGQPDTWNPS
NPGTNANLHVTITSSGQDVGVAAALAKTLEYAAKSGDTASRDLAKGLLDSMW
NNDQDSLGVSTPETRTDYSRFTQVYDPTTGDGLYIPSGWTGTMPNGDQIKPGAT
FLSIRSWYTKDPQWSKVQAYLNNGGPAPTFNYHRFWAESDFAMANADFGMLFPS
G

FIGURE 8A

DNA sequence of *Acidothermus cellulolyticus* GH74 catalytic domain

GCGACGACTCAGCCGTACACCTGGAGCAACGTGGCGATCGGGGGCGGCGGC
TTTGTGACGCGGATCGTCTTCAATGAAGGTGCACCGGGAATTCTGTACGTGCG
GACGGACATCGGGGGGATGTATCGATGGGATGCCGCCAACGGGCGGTGGAT
CCCTCTTCTGGATTGGGTGGGATGGAACAATTGGGGGTACAACGGCGTCGTC
AGCATTGCGGCAGACCCGATCAATACTAACAAGGTATGGGCCGCCGTCGGAA
TGTACACCAACAGCTGGGACCCAAACGACGGAGCGATTCTCCGCTCGTCTGA
TCAGGGCGCAACGTGGCAAATAACGCCCCCTGCCGTTCAAGCTTGGCGGCAAC
ATGCCCCGGGCGTGGAATGGGCGAGCGGCTTGCGGTGGATCCAAACAATGACA
ACATTCTGTATTTTCGGCGCCCCGAGCGGCAAAGGGCTCTGGAGAAGCACAGA
TTCCGGCGCGACCTGGTCCCAGATGACGAACTTTCCGGACGTAGGCACGTAC
ATTGCAAATCCCACTGACACGACCGGCTATCAGAGCGATATTCAAGGCGTCG
TCTGGGTCGCTTTCGACAAGTCTTCGTCATCGCTCGGGCAAGCGAGTAAGACC
ATTTTTGTGGGCGTGCGGATCCCAATAATCCGGTCTTCTGGAGCAGAGACG
GCGGCGCGACGTGGCAGGCGGTGCCGGGTGCGCCGACCGGCTTCATCCCGCA
CAAGGGCGTCTTTGACCCGGTCAACCACGTGCTCTATATTGCCACCAGCAAT
ACGGGTGGTCCGTATGACGGGAGCTCCGGCGACGTCTGGAAATTCTCGGTGA
CCTCCGGGACATGGACGCGAATCAGCCCGGTACCTTCGACGGACACGGCCAA
CGACTACTTTGGTTACAGCGGCCTCACTATCGACCGCCAGCACCCGAACACG
ATAATGGTGGCAACCCAGATATCGTGGTGGCCGGACACCATAATCTTTCGGA
GCACCGACGGCGGTGCGACGTGGACGCGGATCTGGGATTGGACGAGTTATCC
CAATCGAAGCTTGCGATATGTGCTTGACATTTTCGGCGGAGCCTTGGCTGACCT
TCGGCGTACAGCCGAATCCTCCCGTACCGAGTCCGAAGCTCGGCTGGATGGA
TGAAGCGATGGCAATCGATCCGTTCAACTCTGATCGGATGCTCTACGGAACA
GGCGCGACGTTGTACGCAACAAATGATCTCACGAAGTGGGACTCCGGCGGCC
AGATTCATATCGCGCCGATGGTCAAAGGATTGGAGGAGACGGCGGTAAACG
ATCTCATCAGCCCGCGTCTGGCGCCCCGCTCATCAGCGCTCTCGGAGACCTC
GGCGGCTTCACCCACGCCGACGTTACTGCCGTGCCATCGACGATCTTCACGTC

FIGURE 8B

ACCGGTGTTACGACCGGCACCAGCGTCGACTATGCGGAATTGAATCCGTCG
ATCATCGTTCGCGCTGGAAGTTTCGATCCATCGAGCCAACCGAACGACAGGC
ACGTCGCGTTCTCGACAGACGGCGGCAAGAACTGGTTCCAAGGCAGCGAACC
TGGCGGGGTGACGACGGGCGGCACCGTCGCCGCATCGGCCGACGGCTCTCGT
TTCGTCTGGGCTCCCGGCGATCCCGGTCAGCCTGTGGTGTACGCAGTCGGATT
TGGCAACTCCTGGGCTGCTTCGCAAGGTGTTCCCGCCAATGCCCAGATCCGCT
CAGACCGGGTGAATCCAAAGACTTTCTATGCCCTATCCAATGGAACCTTCTAT
CGAAGCACGGACGGCGGCGTGACATTCCAACCGGTCGCGGCCGGTCTTCCGA
GCAGCGGTGCCGTCGGTGTTCATGTTCCACGCGGTGCCTGGAAAAGAAGGCGA
TCTGTGGCTCGCTGCATCGAGCGGGCTTTACCACTCAACCAATGGCGGCAGC
AGTTGGTCTGCAATCACCGGCGTATCCTCCGCGGTGAACGTGGGATTTGGTA
AGTCTGCGCCCGGGTCGTCATACCCAGCCGTCTTTGTCGTCGGCACGATCGGA
GGCGTTACGGGGGCGTACCGCTCCGACGACGGTGGGACGACCTGGGTACGG
ATCAATGATGACCAGCACCAATACGGAAATTGGGGACAAGCAATCACCGGTG
ACCCGCGAATTTACGGGCGGGTGTACATAGGCACGAACGGCCGTGGAATTGT
CTACGGGGACATTGGTGGTGCGCCGTCCGGATCG

FIGURE 9

Amino acid sequence of *Acidothermus cellulolyticus* 74 catalytic domain (741 amino acids)

ATTQPYTWSNVAIGGGGFVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPL
LDWVGWNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQ
GATWQITPLPFKLGGNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDG
ATWSQMTNFPDVGTYIANPTDTTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVG
VADPNNPVFWSRDGGATWQAVPGAPTGFIPHKGVFDPVNHVLYIATSNTGGPY
DGSSGDVWKFSVTSGTWTRISPVPSTDTANDYFGYSGLTIDRQHPNTIMVATQIS
WWPDTHFRSTDGGATWTRIWDWTSYPNRSRLRYVLDISAEPWLTFGVQPNPPVPS
PKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQIHIAPMVKGLE
ETA VNDLISPPSGAPLISALGDLGGFTHADVTA VPSTIFTSPVFTTGTSVDY AELNP
SIIVRAGSFDPPSSQPNDRHVAFSTDGGKNWFQGSEPPGGVTTGGTVAASADGSRFV
WAPGDPGQPVVYAVGFGNSWAASQGV PANAQIRSDRVNPKTFYALSNGTFYRS
TDGGVTFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWS
AITGVSSAVNVGFGKSAPGSSYPAVFVVG TIGGVTGAYRSDDGGTTWVRINDDQ
HQYGNWGQAITGDPRIYGRVYIGTNGRGIVYGDIGGAPSGS

Figure 10

DNA sequence of *Thermobifida fusca* E3 (TfE3) cellulase including the cellulose binding domain - linker - catalytic domain but lacking a TfE3 signal sequence. (1677 bases)

```
GCCGGCTGCTCGGTGGACTACACGGTCAACTCCTGGGGTACCGGGTTCACCG
CCAACGTCACCATCACCAACCTCGGCAGTGCGATCAACGGCTGGACCCTGGA
GTGGGACTTCCCCGGCAACCAGCAGGTGACCAACCTGTGGAACGGGACCTAC
ACCCAGTCCGGGCAGCACGTGTCGGTCAGCAACGCCCCGTACAACGCCTCCA
TCCCGGCCAACGGAACGGTTGAGTTCGGGTTCAACGGCTCCTACTCGGGCAG
CAACGACATCCCCTCCTCCTTCAAGCTGAACGGGGTTACCTGCGACGGCTCG
GACGACCCCGACCCCGAGCCAGCCCTCCCCAGCCCTTCCCCAGCCCCA
CAGACCCGGATGAGCCGGGCGGCCGACCAACCCGCCCACCAACCCCGGCG
AGAAGGTCGACAACCCGTTTCGAGGGCGCCAAGCTGTACGTGAACCCGGTCTG
GTCGGCCAAGGCCGCGCTGAGCCGGGCGGTTCCGCGGTCGCCAACGAGTCC
ACCGCTGTCTGGCTGGACCGTATCGGCGCCATCGAGGGCAACGACAGCCCGA
CCACCGGCTCCATGGGTCTGCGCGACCACCTGGAGGAGGCCGTCCGCCAGTC
CGGTGGCGACCCGCTGACCATCCAGGTCGTCATCTACAACCTGCCCGGCCGC
GACTGCGCCGCGCTGGCCTCCAACGGTGAGCTGGGTCCCGATGAACTCGACC
GCTACAAGAGCGAGTACATCGACCCGATCGCCGACATCATGTGGGACTTCGC
AGACTACGAGAACCTGCGGATCGTCGCCATCATCGAGATCGACTCCCTGCCC
AACCTCGTCACCAACGTGGGCGGGAACGGCGGCACCGAGCTCTGCGCCTACA
TGAAGCAGAACGGCGGCTACGTCAACGGTGTCTGGCTACGCCCTCCGCAAGCT
GGGCGAGATCCCGAACGTCTACAACTACATCGACGCCGCCACCACGGCTGG
ATCGGCTGGGACTCCAACTTCGGCCCCCTCGGTGGACATCTTCTACGAGGCCG
CCAACGCCTCCGGCTCCACCGTGGACTACGTGCACGGCTTCATCTCCAACAC
GGCCAATACTCGGCCACTGTGGAGCCGTACCTGGACGTCAACGGCACCGTT
AACGGCCAGCTCATCCGCCAGTCCAAGTGGGTTGACTGGAACCAAGTACGTCTG
ACGAGCTCTCCTTCGTCCAGGACCTGCGTCAGGCCCTGATCGCCAAGGGCTTC
CGGTCCGACATCGGTATGCTCATCGACACCTCCCGCAACGGCTGGGGTGGCC
CGAACCGTCCGACCGGACCGAGCTCCTCCACCGACCTCAACACCTACGTTGA
CGAGAGCCGTATCGACCGCCGTATCCACCCCGGTAACCTGGTGCAACCAGGCC
GGTGCGGGCCTCGGCGAGCGGCCACGGTCAACCCGGCTCCCGGTGTTGACG
CCTACGTCTGGGTGAAGCCCCCGGGTGAGTCCGACGGCGCCAGCGAGGAGAT
CCCGAACGACGAGGGCAAGGGCTTCGACCGCATGTGCGACCCGACCTACCAG
GGCAACGCCCCGCAACGGCAACAACCCCTCGGGTGCGCTGCCCAACGCCCCCA
TCTCCGGCCACTGGTTCTCTGCCAGTTCCGCGAGCTGCTGGCCAACGCCTAC
CCGCCTCTGTAA
```

Figure 11

Amino acid sequence of the *Thermobifida fusca* E3 - cellulase including the cellulose binding domain - linker - catalytic domain but lacking the Tfe3 signal sequence. (558 amino acids)

AGCSVDYTVNSWGTGFTANVTITNLGSAINGWTLWDFPGNQQTNLWNGTYT
QSGQHVSVSNAFYNASIPANGTVEFGFNGSYSGSNDIPSSFKLNGVTCDGSDDPD
PEPSPSPSPSPPTDPDEPGGPTNPPTNPGEKVDNPFEGAKLYVNPVWSAKAAAE
GGSANESTAVWLDRIGAIEGNDSPPTGSMGLRDHLEEA VRQSGGDPLTIQVVI
YNLPGRDCAALASNGELGPDELDYKSEYIDPLADIMWDFADYENLRIVAIIIDS
LPNLVTNVGGNGGTELCA YMKQNGGYVNGVGYALRKLGEIPNVYNYIDAAHH
GWIGWDSNFGPSVDIFYEAAANASGSTVDYVHGFISNTANYSATVEPYLDVNGTV
NGQLIRQSKWVDWNQYVDELSFVQDLRQALIAKGFRSDIGMLIDTSRNGWGGP
NRPTGPSSSTDLNTYVDESRIIDRIHPGNWCNQAGAGLGERPTVNPAPGVDA YV
WVKPPGESDGASEEIPNDEGKGFD RMC DPTYQGNARNGNNPSGALPNAPISGH
WFSAQFRELLANAYPPL

Figure 12

DNA sequence of *Thermobifida fusca* E5 (TfE5) endoglucanase including the cellulose binding domain - linker and catalytic domain but lacking a TfE5 signal sequence. (1293 bases)

```
GCCGGTCTCACCGCCACAGTCACCAAAGAATCCTCGTGGGACAACGGCTACT
CCGCGTCCGTACCGTCCGCAACGACACCTCGAGCACCGTCTCCCAGTGGGA
GGTCGTCCTCACCCGTGCCCGGCGGCACTACAGTGGCCCAGGTGTGGAACGCC
CAGCACACCAGCAGCGGCAACTCCCACACCTTCACCGGGGTTTCCTGGAACA
GCACCATCCCCGCCCGGAGGCACCGCCTCTTCCGGCTTCATCGCTTCCGGCAGC
GGCGAACCACCCACTGCACCATCAACGGCGCCCCCTGCGACGAAGGCTCCG
AGCCGGGCGGCCCCGGCGGTCCCGGAACCCCTCCCCGACCCCGGCACGCA
GCCCCGCACCGGCACCCCGGTTCGAGCGGTACGGCAAAGTCCAGGTCTGCGGC
ACCCAGTCTGCGACGAGCACGGCAAACCCGGTCCAAGTGCAGGTCTGCGGC
CCCACGGCATCCAGTGGTTCGACCACTGCCTGACCGACAGCTCGCTGGACGC
CCTGGCCTACGACTGGAAGGCCGACATCATCCGCCTGTCCATGTACATCCAG
GAAGACGGCTACGAGACCAACCCGCGCGGGCTTCACCGACCGGATGCACCAG
CTCATCGACATGGCCACGGCGCGCGGCCTGTACGTGATCGTGGACTGGCACA
TCCTCACCCCGGGCGATCCCCACTACAACCTGGACCGGGCCAAGACCTTCTTC
GCGGAAATCGCCCAGCGCCACGCCAGCAAGACCAACGTGCTCTACGAGATCG
CCAACGAACCCAACGGAGTGAGCTGGGCCTCCATCAAGAGCTACGCCGAAG
AGGTCATCCCGGTGATCCGCCAGCGCGACCCCGACTCGGTGATCATCGTGGG
CACCCGCGGTGTCGTCGCTCGGCGTCTCCGAAGGCTCCGGCCCCGCGGAG
ATCGCGGCCAACCCGGTCAACGCCTCCAACATCATGTACGCCTTCCACTTCTA
CGCGGCCTCGCACCGCGACAACCTCAACGCGCTGCGTGAGGCCTCCGAG
CTGTTCCCGGTCTTCGTACCCGAGTTCGGCACCGAGACCTACACCGGTGACG
GCGCCAACGACTTCCAGATGGCCGACCGCTACATCGACCTGATGGCGGAACG
GAAGATCGGGTGGACCAAGTGGAATACTCGGACGACTTCCGTTCCGGCGCG
GTCTTCCAGCCGGGCACCTGCGCGTCCGGCGGCCCCGTGGAGCGGTTCGTGCG
TGAAGGCGTCCGGACAGTGGGTGCGGAGCAAGCTCCAGTCCTGA
```

Figure 13

Amino acid sequence of the *Thermobifida fusca* E5 –cellulase including the cellulose binding domain - linker - catalytic domain but lacking a TfE5 signal sequence. (430 amino acids)

AGLTATVTKESSWDNGYSASVTVRNDTSSTVSQWEVVLTLPGGTTVAQVWNAQ
HTSSGNSHTFTGVSWNSTIPPGGTASSGFIASGSEPTHTCTINGAPCDEGSEPGGP
GGPGTPSPDPGTQPGTGTPVERYGKVQVCGTQLCDEHGNPVQLRGMSTHGIQW
FDHCLTDSSLDALAYDWKADIIRLSMYIQEDGYETNPRGFTDRMHQLIDMATAR
GLYVIVDWHILTPGDPHYNLDRAKTFFAEIAQRHASKTNVLYEIANEPNGVSWA
SIKSYAEEVIPVIRQRPDSVIIVGTRGWSSLGVSEGSGPAEIAANPVNASNIMYAF
HFYAASHRDNYLNALREASELFPVFEFGTETTYTGDGANDFQMADRYIDLMA
ERKIGWTKWNYSDDFRSGAVFQPGTCASGGPWSSSLKASGQWVRSLQS

Figure 14

DNA sequence of CBH1-E1 fusion (2656 bases)

T.reesei cbh1 signal sequence+catalytic domain+linker+added amino acidsSKR+*Acidothermus cellulolyticus* GH5A catalytic domain

ATGTATCGGAAGTTGGCCGTCATCTCGGCCTTCTTGGCCACAGCTCGTGCTCA
GTCGGCCTGCACTCTCCAATCGGAGACTCACCCGCCTCTGACATGGCAGAAA
TGCTCGTCTGGTGGCACTTGCACTCAACAGACAGGCTCCGTGGTCATCGACG
CCAACTGGCGCTGGACTCACGCTACGAACAGCAGCACGAACTGCTACGATGG
CAACACTTGAGCTCGACCCTATGTCCTGACAACGAGACCTGCGCGAAGAAC
TGCTGTCTGGACGGTGCCGCCTACGCGTCCACGTACGGAGTTACCACGAGCG
GTAACAGCCTCTCCATTGGCTTTGTACCCAGTCTGCGCAGAAGAACGTTGGC
GCTCGCCTTTACCTTATGGCGAGCGACACGACCTACCAGGAATTCACCCTGCT
TGGCAACGAGTTCTCTTTCGATGTTGATGTTTCGCAGCTGCCGTAAGTGACTT
ACCATGAACCCCTGACGTATCTTCTTGTGGGCTCCCAGCTGACTGGCCAATTT
AAGGTGCGGCTTGAACGGAGCTCTCTACTTCGTGTCCATGGACGCGGATGGT
GGCGTGAGCAAGTATCCCAACACACCGCTGGCGCCAAGTACGGCACGGGGT
ACTGTGACAGCCAGTGTCCCCGCGATCTGAAGTTCATCAATGGCCAGGCCAA
CGTTGAGGGCTGGGAGCCGTCATCCAACAACGCAAACACGGGCATTGGAGG
ACACGGAAGCTGCTGCTCTGAGATGGATATCTGGGAGGCCAACTCCATCTCC
GAGGCTCTTACCCCCCACCCTTGCACGACTGTCGGCCAGGAGATCTGCGAGG
GTGATGGGTGCGGCGGAACCTTACTCCGATAACAGATATGGCGGCACTTGCGA
TCCCGATGGCTGCGACTGGAACCCATACCGCCTGGGCAACACCAGCTTCTAC
GGCCCTGGCTCAAGCTTTACCCTCGATACCACCAAGAAATTGACCGTTGTCAC
CCAGTTCGAGACGTCGGGTGCCATCAACCGATACTATGTCCAGAATGGCGTC
ACTTTCCAGCAGCCCAACGCCGAGCTTGGTAGTTACTCTGGCAACGAGCTCA
ACGATGATTACTGCACAGCTGAGGAGGCAGAATTCGGCGGATCCTCTTTCTC
AGACAAGGGCGGCCTGACTCAGTTCAAGAAGGCTACCTCTGGCGGCATGGTT
CTGGTCATGAGTCTGTGGGATGATGTGAGTTTGATGGACAAACATGCGCGTT
GACAAAGAGTCAAGCAGCTGACTGAGATGTTACAGTACTACGCCAACATGCT
GTGGCTGGACTCCACCTACCCGACAAACGAGACCTCCTCCACACCCGGTGCC
GTGCGCGGAAGCTGCTCCACCAGCTCCGGTGTCCCTGCTCAGGTGCAATCTC
AGTCTCCCAACGCCAAGGTCACCTTCTCCAACATCAAGTTCGGACCCATTGGC
AGCACCGGCAACCCTAGCGGCGGCAACCCTCCCGGCGGAAACCCGCCTGGCA
CCACCACCACCCGCCGCCAGCCACTACCACTGGAAGCTCTCCCGGACCTAC
TAGTAAGCGGGCGGGCGGGCGGCTATTGGCACACGAGCGGCCGGGAGATCCT
GGACGCGAACAACGTGCCGGTACGGATCGCCGGCATCAACTGGTTTGGGTTT
GAAACCTGCAATTACGTTCGTGCACGGTCTCTGGTCACGCGACTACCGCAGCA
TGCTCGACCAGATAAAGTCGCTCGGCTACAACACAATCCGGCTGCCGTACTC
TGACGACATTCTCAAGCCGGGCACCATGCCGAACAGCATCAATTTTACCAG
ATGAATCAGGACCTGCAGGGTCTGACGTCCTTGCAGGTCATGGACAAAATCG
TCGCGTACGCCGGTCAGATCGGCCTGCGCATCATTCTTGACCGCCACCGACC
GGATTGCAGCGGGCAGTCGGCGCTGTGGTACACGAGCAGCGTCTCGGAGGCT
ACGTGGATTTCGACCTGCAAGCGCTGGCGCAGCGCTACAAGGGAAACCCGA

CGGTCGTCGGCTTTGACTTGCACAACGAGCCGCATGACCCGGCCTGCTGGGG
CTGCGGCGATCCGAGCATCGACTGGCGATTGGCCGCCGAGCGGGCCGGAAC
GCCGTGCTCTCGGTGAATCCGAACCTGCTCATTTTCGTCGAAGGTGTGCAGAG
CTACAACGGAGACTCCTACTGGTGGGGCGGCAACCTGCAAGGAGCCGGCCA
GTACCCGGTCGTGCTGAACGTGCCGAACCGCCTGGTGTACTCGGCGCACGAC
TACGCGACGAGCGTCTACCCGCAGACGTGGTTCAGCGATCCGACCTTCCCCA
ACAACATGCCCCGGCATCTGGAACAAGAACTGGGGATACCTCTTCAATCAGAA
CATTGCACCGGTATGGCTGGGCGAATTCGGTACGACACTGCAATCCACGACC
GACCAGACGTGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCGCAAT
ACGGTGCGGACAGCTTCCAGTGGACCTTCTGGTCCTGGAACCCCGATTCCGG
CGACACAGGAGGAATTCTCAAGGATGACTGGCAGACGGTCGACACAGTAAA
AGACGGCTATCTCGCGCCGATCAAGTCGTTCGATTTTCGATCCTGTCGGCTAA

Figure 15

Amino acid sequence of CBH1-E1 fusion (841 amino acids)

Treesei cbh1 signal sequence+catalytic domain+linker+added amino acids

SKR+*Acidothermus cellulolyticus* GH5A catalytic domain

MYRKLAVISAFLATARAQSACTLQSETHPPLTWQKCSSGGTCTQQTGSVVIDAN
WRWTHATNSSTNCYDGNTWSSTLCPDNETCAKNCCLDGAAYASTYGVTTSGNS
LSIGFVTQSAQKNVGARLYLMASDTTYQEFTLLGNEFSFDVDVSQLPCGLNGAL
YFVSMDADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQANVEGWEPSSN
NANTGIGGHGSCCSEMDIWEANSISEALTPHPCTTVGQEICEGDGCGGTYSNRY
GGTCDPDGCDWNPYRLGNTSFYGPSSFTLDTTKKLTVVVTQFETSGAINRYVQ
NGVTFQQPNAELGSYSGNELNDDYCTAEAEFGSSFSKGGGLTQFKKATSGGM
VLVMSLWDDYYANMLWLDSTYPTNETSSTPGAVRGSCSTSSGVPAQVESQSPN
AKVTFSNIKFGPIGSTGNPSGGNPPGGNPPGTTTTTRRPATTTGSSPGPTSKRAGG
YWHTSGREILDANNVPVRIAGINWFGFETCNVYVHGLWSRDYRSMLDQIKSLGY
NTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGLRILD
RHRPDCSGQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEPHDPAC
WCGGDPSIDWRLAAERAGNAVLSVNPPLLIFVEGVQSYNGDSYWWGGNLQGA
GQYPVVLNVPNRLVYSAHDYATSVYPQTFWSDPTFPNNMPGIWNKNWGYLFN
QNIAPVWLGEFGTTLQSTTDQTLWKLTVQYLRPTAQYGADSFQWTFWSWNPDS
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Figure 16

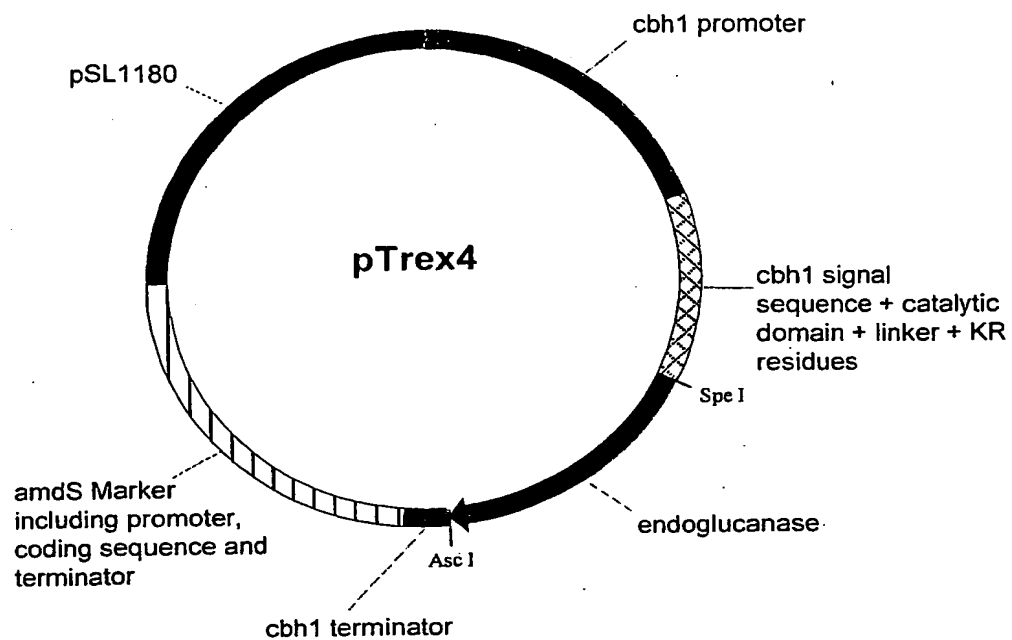


Figure 17

DNA sequence of pTrex4 (10239 bases)

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GAATTCTCACGGTGAATGTAGGCCTTTTGTAGGGTAGGAATTGTCACTCAAGC
ACCCCCAACCTCCATTACGCCTCCCCCATAGAGTTCCCAATCAGTGAGTCATG
GCACTGTTCTCAAATAGATTGGGGGAGAAGTTGACTTCCGCCCAGAGCTGAAG
GTCGCACAACCGCATGATATAGGGTCGGCAACGGCAAAAAAGCACGTGGCT
CACCGAAAAGCAAGATGTTTGCGATCTAACATCCAGGAACCTGGATACATCC
ATCATCACGCACGACCACTTTGATCTGCTGGTAAACTCGTATTCGCCCTAAAC
CGAAGTGACGTGGTAAATCTACACGTGGGCCCTTTTCGGTATACTGCGTGTGT
CTTCTCTAGGTGCCATTCTTTTCCCTTCCTCTAGTGTTGAATTGTTTGTGTTGG
AGTCCGAGCTGTAACCTCTGAATCTCTGGAGAATGGTGGACTAACGACT
ACCGTGACCTGCATCATGTATATAATAGTGATCCTGAGAAGGGGGGTTTGG
AGCAATGTGGGACTTTGATGGTCATCAAACAAAGAACGAAGACGCCTCTTTT
GCAAAGTTTTGTTTCGGCTACGGTGAAGAACTGGATACTTGTTGTGTCTTCTG
TGTATTTTTGTGGCAACAAGAGGCCAGAGACAATCTATTCAAACACCAAGCT
TGCTCTTTTGAGCTACAAGAACCTGTGGGGTATATATCTAGAGTTGTGAAGTC
GGTAATCCCGCTGTATAGTAATACGAGTCGCATCTAAATACTCCGAAGCTGCT
GCGAACCCGGAGAATCGAGATGTGCTGGAAAGCTTCTAGCGAGCGGCTAAAT
TAGCATGAAAGGCTATGAGAAATTCTGGAGACGGCTTGTTGAATCATGGCGT
TCCATTCTTCGACAAGCAAAGCGTTCCGTCGCAGTAGCAGGCACTCATTCCCG
AAAAAACTCGGAGATTCCTAAGTAGCGATGGAACCGGAATAATATAATAGGC
AATACATTGAGTTGCCTCGACGGTTGCAATGCAGGGGTACTGAGCTTGGACA
TAACTGTTCCGTACCCACCTCTTCTCAACCTTTGGCGTTTCCCTGATTCAGCG
TACCCGTACAAGTCGTAATCACTATTAACCCAGACTGACCGGACGTGTTTTGC
CCTTCATTTGGAGAAATAATGTCATTGCGATGTGTAATTTGCCTGCTTGACCG
ACTGGGGCTGTTGGAAGCCCGAATGTAGGATTGTTATCCGAACCTCTGCTCGTA
GAGGCATGTTGTGAATCTGTGTCTGGGCAGGACACGCCTCGAAGGTTACGGC

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TGGGTCGCTTGTCTTCCGGTGAAGTGAAAGAAGACAGAGGTAAGAATGTC
TGA CTCGGAGCGTTTTGCATACAACCAAGGGCAGTGATGGAAGACAGTGAAA
TGTTGACATTCAAGGAGTATTTAGCCAGGGATGCTTGAGTGTATCGTGTAAG
GAGGTTTGTCTGCCGATACGACGAATACTGTATAGTCACTTCTGATGAAGTGG
TCCATATTGAAATGTAAGTCGGCACTGAACAGGCAAAAGATTGAGTTGAAAC
TGCCTAAGATCTCGGGCCCTCGGGCCTTCGGCCTTTGGGTGTACATGTTTGTG
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AGCAGCTGAGGGTATGTGATAGGCAAATGTTCAAGGGGCCACTGCATGGTTTC
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TCGAGGTCCGTGCCTCCCTCATGCTCTCCCCATCTACTCATCAACTCAGATCC
TCCAGGAGACTTGTACACCATCTTTTGAGGCACAGAAACCCAATAGTCAACC
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GACATGGCAGAAATGCTCGTCTGGTGGCACTTGCACTCAACAGACAGGCTCC
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CTGCGGAAGAACTGCTGTCTGGACGGTGCCGCCTACGCGTCCACGTACGGA
GTTACCACGAGCGGTAACAGCCTCTCCATTGGCTTTGTCACCCAGTCTGCGCA
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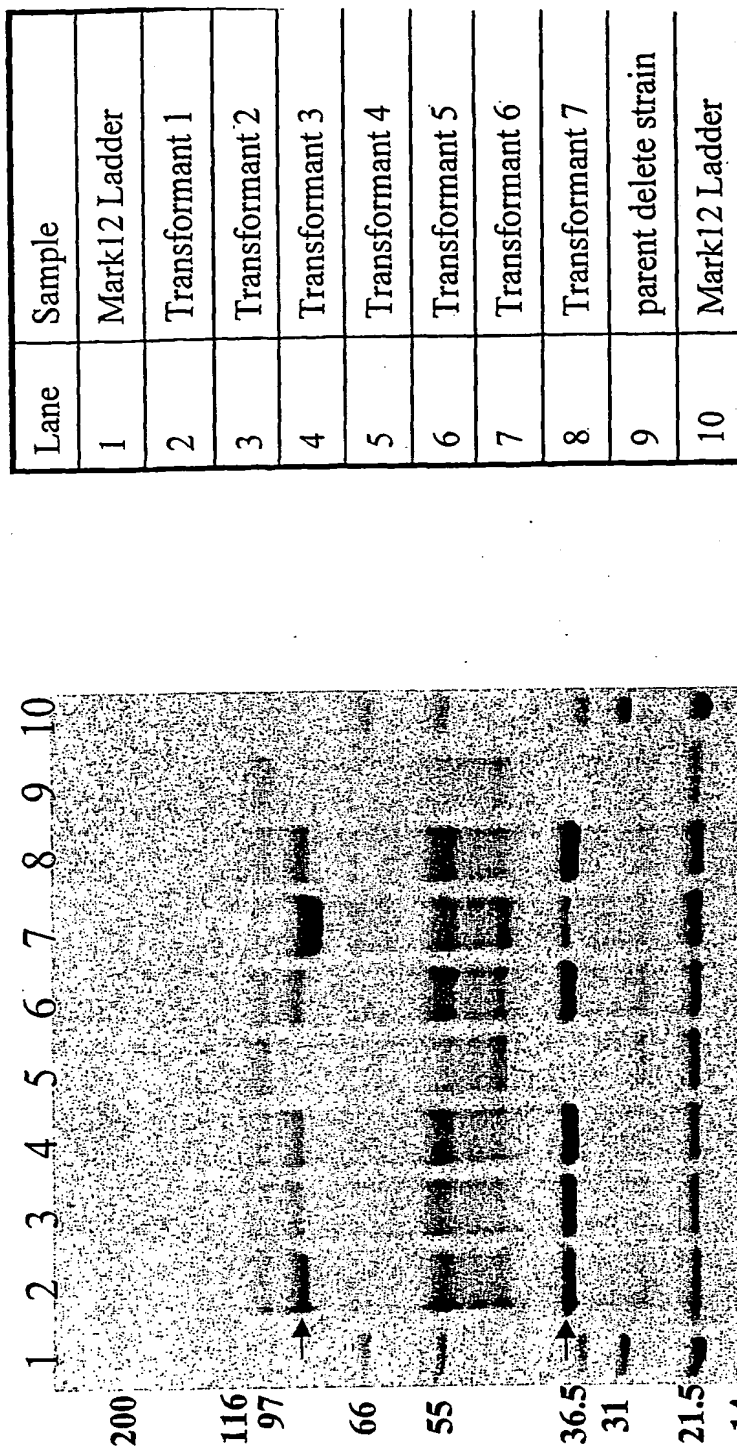
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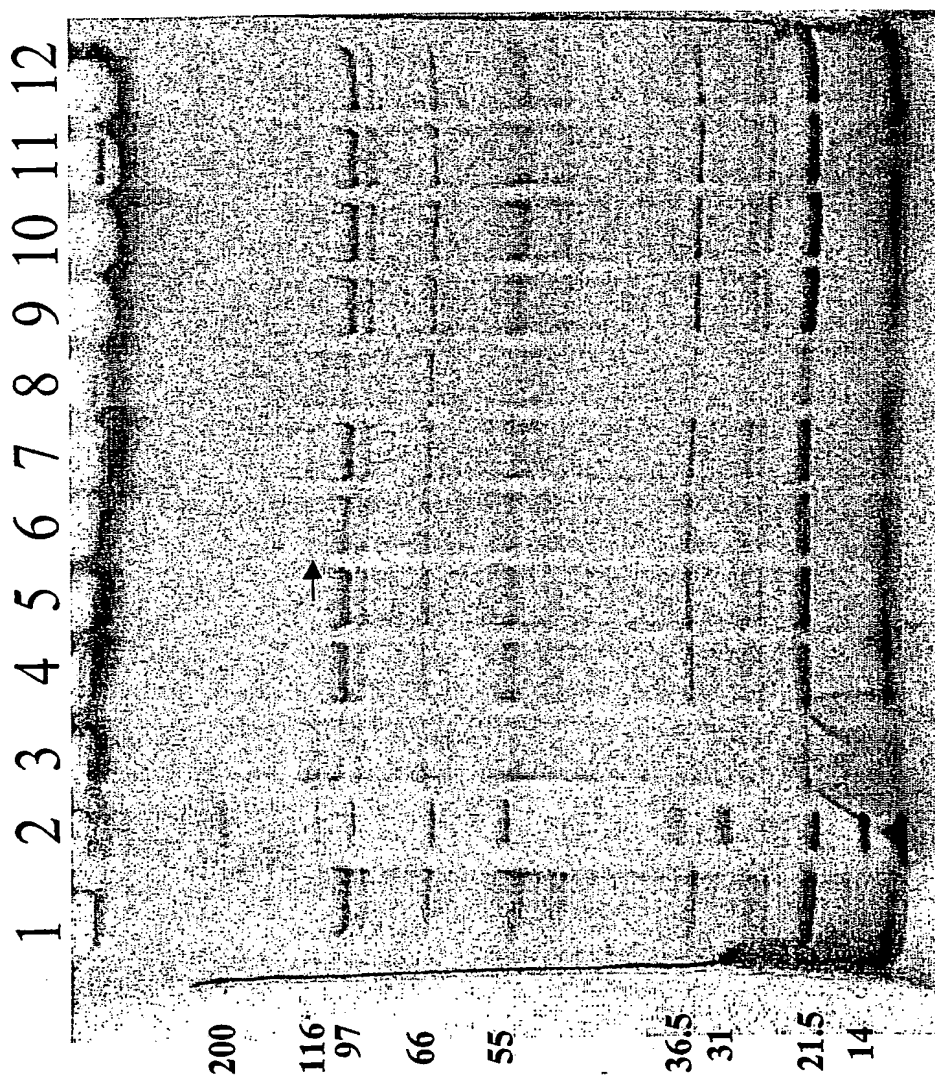
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TTCCAGTCACGACGTTGTAAAACGACGGCCAGTGCC

Figure 18
 SDS-PAGE gel of supernate samples of shake flask grown *T.reesei* delete strain
 transformed with the fusion expression construct *cbh1-E1*



The fusion protein is indicated by the upper arrow, the
 cleaved E1 catalytic domain is indicated by the lower arrow

Figure 19
SDS-PAGE gel of supernate samples of shake flask grown *T.reesei* delete strain transformed with the fusion expression construct *cbh1-GH48*

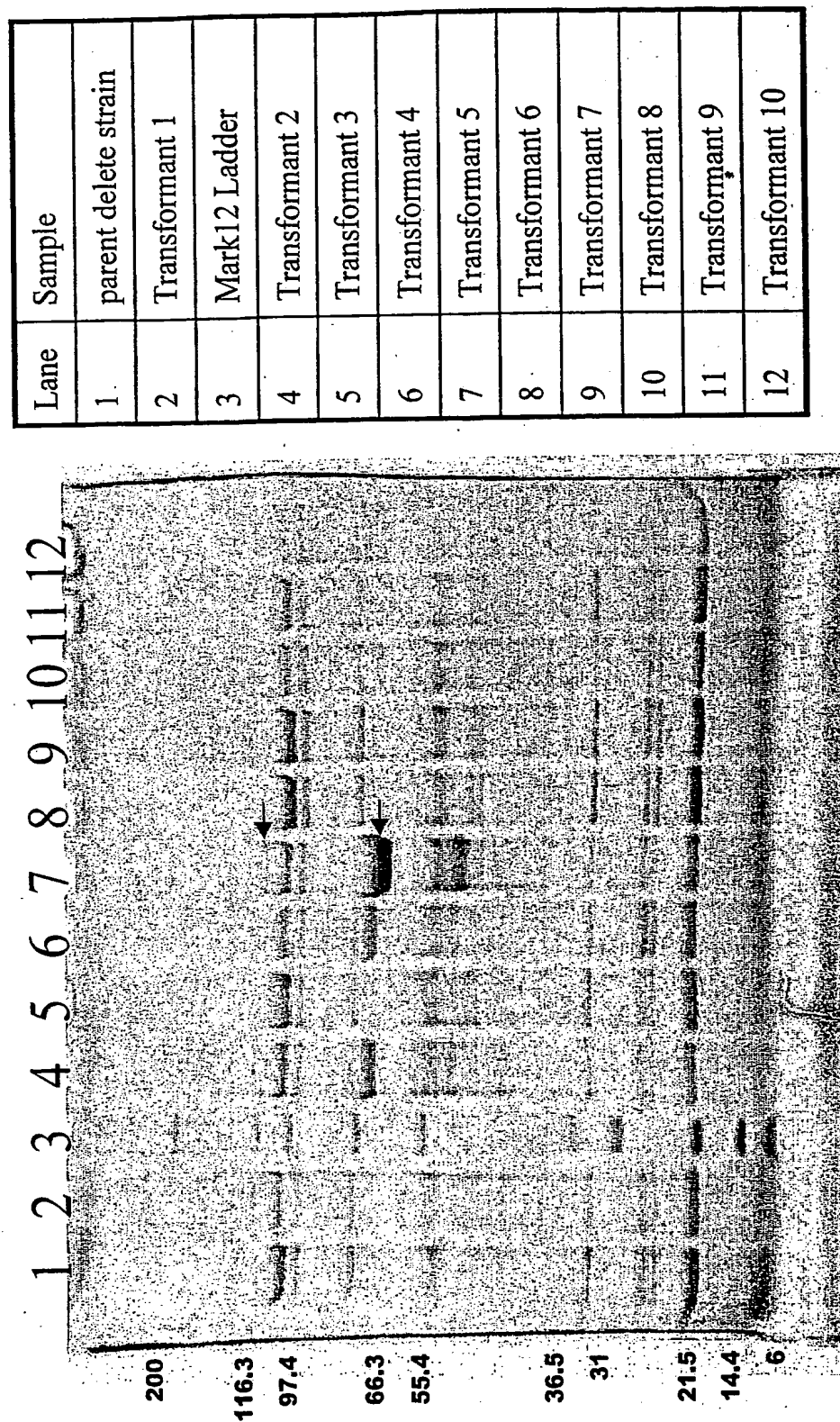


The fusion protein is indicated by the arrow

Lane	Sample
1	parent delete strain
2	Mark12 Ladder
3	Transformant 1
4	Transformant 2
5	Transformant 3
6	Transformant 4
7	Transformant 5
8	Transformant 6
9	Transformant 7
10	Transformant 8
11	Transformant 9
12	Transformant 10

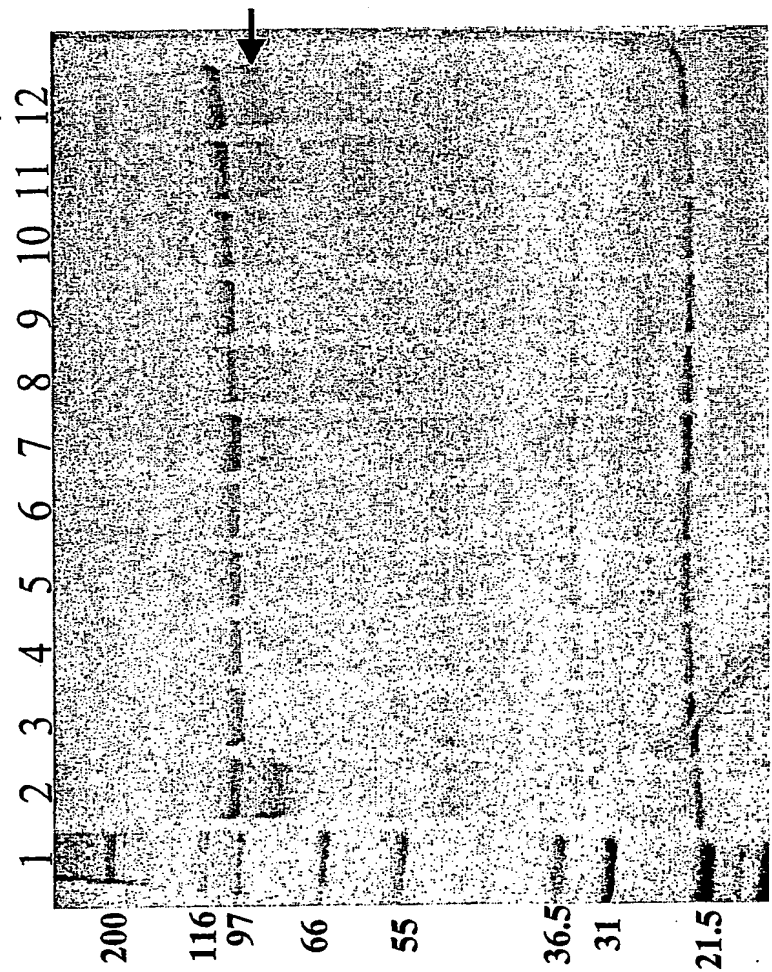
Figure 20

SDS-PAGE gel of supernate samples of shake flask grown *T. reesei* delete strain transformed with the fusion expression construct *cbh1-GH74*



The fusion protein is indicated by the upper arrow, the cleaved GH74 catalytic domain is indicated by the lower arrow

Figure 21
SDS-PAGE gel of supernate samples of shake flask grown *T.reesei* delete strain transformed with the fusion expression construct *cbh1-E3*

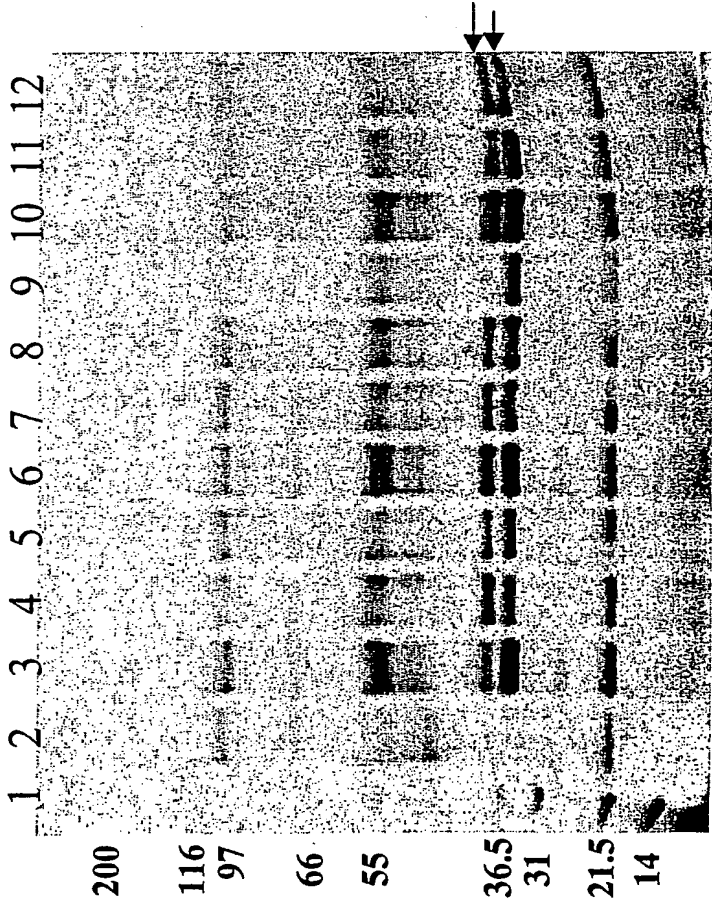


arrow indicates new protein expressed
in *cbh1-E3* transformants

Lane	Sample
1	Mark12 Ladder
2	Transformant 1
3	Transformant 2
4	Transformant 3
5	Transformant 4
6	Transformant 5
7	Transformant 6
8	Transformant 7
9	Transformant 8
10	Transformant 9
11	Transformant 10
12	Transformant 11

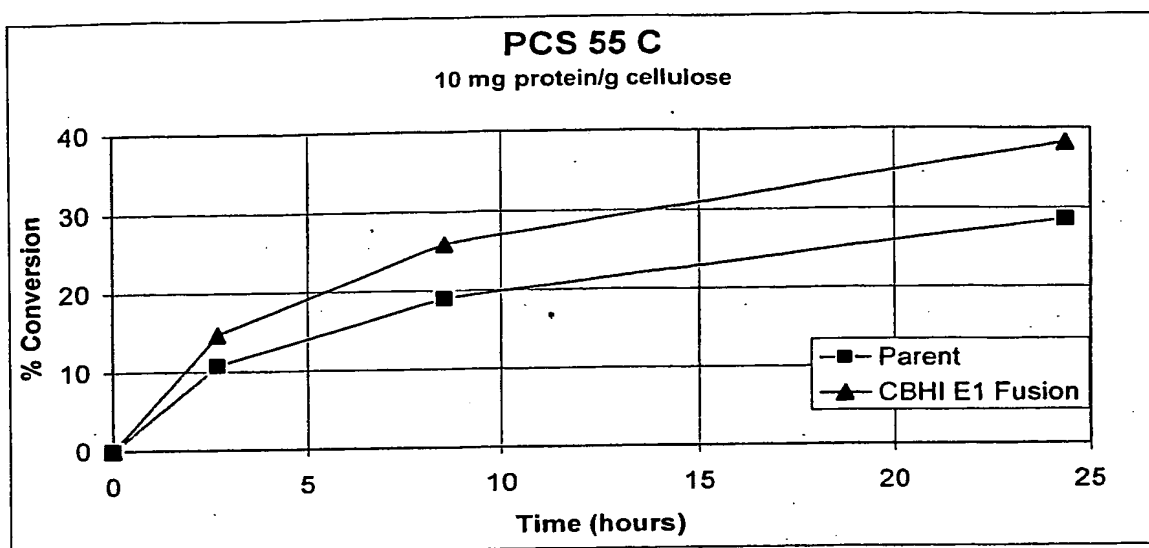
Figure 22
SDS-PAGE gel of supernate samples of shake flask grown *T.reesei* delete strain transformed with the fusion expression construct cbh1-E5

Lane	Sample
1	Mark12 Ladder
2	parent delete strain
3	Transformant 1
4	Transformant 2
5	Transformant 3
6	Transformant 4
7	Transformant 5
8	Transformant 6
9	Transformant 7
10	Transformant 8
11	Transformant 9
12	Transformant 10



E5 is indicated by the lower arrows

FIGURE 23



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